

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 09/881,736A  
Source: 1FW16  
Date Processed by STIC: 12/20/04

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IFW16

## RAW SEQUENCE LISTING

DATE: 12/20/2004

PATENT APPLICATION: US/09/881,736A

TIME: 12:22:01

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Output Set: N:\CRF4\12202004\I881736A.raw

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4 <110> APPLICANT: Glotzer, Michael
5      Jantsch-Plunger, Verena
6      Romano, Alper
7      Mishima, Masanori
8      Kaitna, Susanne
10 <120> TITLE OF INVENTION: Cyk-4 polypeptides, DNA molecules encoding them and their
use in screening
11      methods
13 <130> FILE REFERENCE: 0652.2260001/EKS/AES
15 <140> CURRENT APPLICATION NUMBER: US 09/881,736A
16 <141> CURRENT FILING DATE: 2001-06-18
18 <150> PRIOR APPLICATION NUMBER: EP 00 112 880.0
19 <151> PRIOR FILING DATE: 2000-06-19
21 <150> PRIOR APPLICATION NUMBER: EP 01 110 554.1
22 <151> PRIOR FILING DATE: 2001-04-30
24 <150> PRIOR APPLICATION NUMBER: 60/241,231
25 <151> PRIOR FILING DATE: 2000-10-18
27 <150> PRIOR APPLICATION NUMBER: To be determined
28 <151> PRIOR FILING DATE: 2001-06-13
31 <160> NUMBER OF SEQ ID NOS: 8
33 <170> SOFTWARE: PatentIn Ver. 2.1
37 <210> SEQ ID NO: 1
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39 <212> TYPE: DNA
40 <213> ORGANISM: Homo sapiens
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44 <222> LOCATION: (1)..(70)
46 <220> FEATURE:
47 <221> NAME/KEY: CDS
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50 <220> FEATURE:
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52 <222> LOCATION: (1970)..(3050)
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58 cgtgtgaaag atg gat act atg atg ctg aat gtg cgg aat ctg ttt gag 109
59      Met Asp Thr Met Met Leu Asn Val Arg Asn Leu Phe Glu
60      1          5          10
62 cag ctt gtg cgc cgg gtg gag att ctc agt gaa gga aat gaa gtc caa 157
63 Gln Leu Val Arg Arg Val Glu Ile Leu Ser Glu Gly Asn Glu Val Gln
64      15          20          25
66 ttt atc cag ttg gcg aag gac ttt gag gat ttc cgt aaa aag tgg cag 205
67 Phe Ile Gln Leu Ala Lys Asp Phe Glu Asp Phe Arg Lys Lys Trp Gln

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71	Arg	Thr	Asp	His	Glu	Leu	Gly	Lys
72					50		55	
74	gag	act	gag	cga	agt	gct	ctg	gat
75	Glu	Thr	Glu	Arg	Ser	Ala	Leu	Asp
76					65		70	
78	cag	gtg	gat	gta	gag	atc	aaa	cgg
79	Gln	Val	Asp	Val	Glu	Ile	Lys	Arg
80					80		85	
82	gaa	aag	ctg	gaa	cga	cag	att	cag
83	Glu	Lys	Leu	Glu	Arg	Gln	Ile	Gln
84					95		100	
86	gac	aca	tct	ggc	agc	att	caa	cta
87	Asp	Thr	Ser	Gly	Ser	Ile	Gln	Leu
88	110				115		120	
90	gct	ttt	ctc	aac	aga	ggc	caa	cca
91	Ala	Phe	Leu	Asn	Arg	Gly	Gln	Pro
92					130		135	
94	aga	cta	tca	acc	att	gat	gaa	tct
95	Arg	Leu	Ser	Thr	Ile	Asp	Glu	Ser
96					145		150	
98	ttt	gac	aag	act	gat	gaa	tca	ctg
99	Phe	Asp	Lys	Thr	Asp	Glu	Ser	Leu
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102	act	ttc	aaa	ctg	aag	aag	aga	gaa
103	Thr	Phe	Lys	Leu	Lys	Lys	Arg	Glu
104					175		180	
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107	Phe	Val	Asp	Gly	Pro	Pro	Gly	Pro
108	190				195		200	
110	tct	gca	gta	gac	cag	ggg	aat	gaa
111	Ser	Ala	Val	Asp	Gln	Gly	Asn	Glu
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114	act	gtt	ccc	aat	gat	ggc	ggg	ccc
115	Thr	Val	Pro	Asn	Asp	Gly	Gly	Pro
116					225		230	
118	act	gtg	cca	tat	tgg	acc	agg	agc
119	Thr	Val	Pro	Tyr	Trp	Thr	Arg	Ser
120					240		245	
122	cct	tgg	aac	agt	gac	tcc	acc	ctg
123	Pro	Trp	Asn	Ser	Asp	Ser	Thr	Leu
124					255		260	
126	act	gag	aca	gac	agt	gtg	ggc	acg
127	Thr	Glu	Thr	Asp	Ser	Val	Gly	Thr
128	270				275		280	
130	ctg	cat	gac	ttt	gtt	tct	aag	acg
131	Leu	His	Asp	Phe	Val	Ser	Lys	Thr
132					290		295	

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134 cca tgt gga aag cgg ata aaa ttt ggc aaa tta tct ctg aag tgt cga 1021
135 Pro Cys Gly Lys Arg Ile Lys Phe Gly Lys Leu Ser Leu Lys Cys Arg
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138 gac tgt cgt gtg gtc tct cat cca gaa tgt cgg gac cgc tgt ccc ctt 1069
139 Asp Cys Arg Val Val Ser His Pro Glu Cys Arg Asp Arg Cys Pro Leu
140          320          325          330
142 ccc tgc att cct acc ctg ata gga aca cct gtc aag att gga gag gga 1117
143 Pro Cys Ile Pro Thr Leu Ile Gly Thr Pro Val Lys Ile Gly Glu Gly
144          335          340          345
146 atg ctg gca gac ttt gtg tcc cag act tct cca atg atc ccc tcc att 1165
147 Met Leu Ala Asp Phe Val Ser Gln Thr Ser Pro Met Ile Pro Ser Ile
148 350          355          360          365
150 gtt gtg cat tgt gta aat gag att gag caa aga ggt ctg act gag aca 1213
151 Val Val His Cys Val Asn Glu Ile Glu Gln Arg Gly Leu Thr Glu Thr
152          370          375          380
154 ggc ctg tat agg atc tct ggc tgt gac cgc aca gta aaa gag ctg aaa 1261
155 Gly Leu Tyr Arg Ile Ser Gly Cys Asp Arg Thr Val Lys Glu Leu Lys
156          385          390          395
158 gag aaa ttc ctc aga gtg aaa act gta ccc ctc ctc agc aaa gtg gat 1309
159 Glu Lys Phe Leu Arg Val Lys Thr Val Pro Leu Leu Ser Lys Val Asp
160          400          405          410
162 gat atc cat gct atc tgt agc ctt cta aaa gac ttt ctt cga aac ctc 1357
163 Asp Ile His Ala Ile Cys Ser Leu Leu Lys Asp Phe Leu Arg Asn Leu
164          415          420          425
166 aaa gaa cct ctt ctg acc ttt cgc ctt aac aga gcc ttt atg gaa gca 1405
167 Lys Glu Pro Leu Leu Thr Phe Arg Leu Asn Arg Ala Phe Met Glu Ala
168 430          435          440          445
170 gca gaa atc aca gat gaa gac aac agc ata gct gcc atg tac caa gct 1453
171 Ala Glu Ile Thr Asp Glu Asp Asn Ser Ile Ala Ala Met Tyr Gln Ala
172          450          455          460
174 gtt ggt gaa ctg ccc cag gcc aac agg gac aca tta gct ttc ctc atg 1501
175 Val Gly Glu Leu Pro Gln Ala Asn Arg Asp Thr Leu Ala Phe Leu Met
176          465          470          475
178 att cac ttg cag aga gtg gct cag agt cca cat act aaa atg gat gtt 1549
179 Ile His Leu Gln Arg Val Ala Gln Ser Pro His Thr Lys Met Asp Val
180          480          485          490
182 gcc aat ctg gct aaa gtc ttt ggc cct aca ata gtg gcc cat gct gtg 1597
183 Ala Asn Leu Ala Lys Val Phe Gly Pro Thr Ile Val Ala His Ala Val
184          495          500          505
186 ccc aat cca gac cca gtg aca atg tca cag gac atc aag cgt caa ccc 1645
187 Pro Asn Pro Asp Pro Val Thr Met Ser Gln Asp Ile Lys Arg Gln Pro
188 510          515          520          525
190 aag gtg gtt gag cgc ctg ctt tcc ttg cct ctg gag tat tgg agt cag 1693
191 Lys Val Val Glu Arg Leu Leu Ser Leu Pro Leu Glu Tyr Trp Ser Gln
192          530          535          540
194 ttc atg atg gtg gag caa gag aac att gac ccc cta cat gtc att gaa 1741
195 Phe Met Met Val Glu Gln Glu Asn Ile Asp Pro Leu His Val Ile Glu
196          545          550          555
198 aac tca aat gcc ttt tca aca cca cag aca cca gat att aaa gtg agt 1789

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202 tta ctg gga cct gtg acc act cct gaa cat cag ctt ctc aag act cct 1837
203 Leu Leu Gly Pro Val Thr Thr Pro Glu His Gln Leu Leu Lys Thr Pro
204      575      580      585
206 tca tct agt tcc ctg tca cag aga gtc cgt tcc acc ctc acc aag aac 1885
207 Ser Ser Ser Ser Leu Ser Gln Arg Val Arg Ser Thr Leu Thr Lys Asn
208 590      595      600      605
210 act cct aga ttt ggg agc aaa agc aag tct gcc act aac cta gga cga 1933
211 Thr Pro Arg Phe Gly Ser Lys Ser Lys Ser Ala Thr Asn Leu Gly Arg
212      610      615      620
214 caa ggc aac ttt ttt gct tct cca atg ctc aag tga agtcacatct 1979
215 Gln Gly Asn Phe Phe Ala Ser Pro Met Leu Lys
216      625      630
218 gcctgttact tcccagcatt gactgactat aagaaaggac acatctgtac tctgctctgc 2039
220 agcctcctgt actcattact acttttagca ttctccaggc ttttactcaa gtttaattgt 2099
222 gcatgagggt tttattaaaa ctatatatat ctccccttcc ttctcctcaa gtcacataat 2159
224 atcagcactt tgtgctggtc attggttgga gcttttagat gagacatctt tccaggggta 2219
226 gaagggttag tatggaattg gttgtgattc tttttgggga aggggggttat tgttcctttg 2279
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242 aaaattgaat tcattctgat gcttggtccc cataccccc accttgtcca gtggagccca 2759
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248 tggatgctga aatttttccc atggaacata gccacatcta gatagatgtg agctttttct 2939
250 tctgttaaaa ttattcttaa tgtctgtaaa aacgattttc ttctgtagaa tgtttgactt 2999
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267      20      25      30
269 Leu Ala Lys Asp Phe Glu Asp Phe Arg Lys Lys Trp Gln Arg Thr Asp
270      35      40      45
272 His Glu Leu Gly Lys Tyr Lys Asp Leu Leu Met Lys Ala Glu Thr Glu
273      50      55      60
275 Arg Ser Ala Leu Asp Val Lys Leu Lys His Ala Arg Asn Gln Val Asp
276 65      70      75      80
278 Val Glu Ile Lys Arg Arg Gln Arg Ala Glu Ala Asp Cys Glu Lys Leu
279      85      90      95

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284 Gly Ser Ile Gln Leu Ser Glu Glu Gln Lys Ser Ala Leu Ala Phe Leu
285           115           120           125
287 Asn Arg Gly Gln Pro Ser Ser Ser Asn Ala Gly Asn Lys Arg Leu Ser
288       130           135           140
290 Thr Ile Asp Glu Ser Gly Ser Ile Leu Ser Asp Ile Ser Phe Asp Lys
291 145           150           155           160
293 Thr Asp Glu Ser Leu Asp Trp Asp Ser Ser Leu Val Lys Thr Phe Lys
294           165           170           175
296 Leu Lys Lys Arg Glu Lys Arg Arg Ser Thr Ser Arg Gln Phe Val Asp
297           180           185           190
299 Gly Pro Pro Gly Pro Val Lys Lys Thr Arg Ser Ile Gly Ser Ala Val
300           195           200           205
302 Asp Gln Gly Asn Glu Ser Ile Val Ala Lys Thr Thr Val Thr Val Pro
303       210           215           220
305 Asn Asp Gly Gly Pro Ile Glu Ala Val Ser Thr Ile Glu Thr Val Pro
306 225           230           235           240
308 Tyr Trp Thr Arg Ser Arg Arg Lys Thr Gly Thr Leu Gln Pro Trp Asn
309           245           250           255
311 Ser Asp Ser Thr Leu Asn Ser Arg Gln Leu Glu Pro Arg Thr Glu Thr
312           260           265           270
314 Asp Ser Val Gly Thr Pro Gln Ser Asn Gly Gly Met Arg Leu His Asp
315           275           280           285
317 Phe Val Ser Lys Thr Val Ile Lys Pro Glu Ser Cys Val Pro Cys Gly
318       290           295           300
320 Lys Arg Ile Lys Phe Gly Lys Leu Ser Leu Lys Cys Arg Asp Cys Arg
321 305           310           315           320
323 Val Val Ser His Pro Glu Cys Arg Asp Arg Cys Pro Leu Pro Cys Ile
324           325           330           335
326 Pro Thr Leu Ile Gly Thr Pro Val Lys Ile Gly Glu Gly Met Leu Ala
327           340           345           350
329 Asp Phe Val Ser Gln Thr Ser Pro Met Ile Pro Ser Ile Val Val His
330           355           360           365
332 Cys Val Asn Glu Ile Glu Gln Arg Gly Leu Thr Glu Thr Gly Leu Tyr
333       370           375           380
335 Arg Ile Ser Gly Cys Asp Arg Thr Val Lys Glu Leu Lys Glu Lys Phe
336 385           390           395           400
338 Leu Arg Val Lys Thr Val Pro Leu Leu Ser Lys Val Asp Asp Ile His
339           405           410           415
341 Ala Ile Cys Ser Leu Leu Lys Asp Phe Leu Arg Asn Leu Lys Glu Pro
342           420           425           430
344 Leu Leu Thr Phe Arg Leu Asn Arg Ala Phe Met Glu Ala Ala Glu Ile
345           435           440           445
347 Thr Asp Glu Asp Asn Ser Ile Ala Ala Met Tyr Gln Ala Val Gly Glu
348       450           455           460
350 Leu Pro Gln Ala Asn Arg Asp Thr Leu Ala Phe Leu Met Ile His Leu
351 465           470           475           480
353 Gln Arg Val Ala Gln Ser Pro His Thr Lys Met Asp Val Ala Asn Leu

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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

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**VERIFICATION SUMMARY**

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